

SEQUENCE LISTING

<110> Shorrosh, Basil S.
DeBonte, Lorin R.

<120> PLANTS CONTAINING A CYTOSOLIC ACETYL
COA-CARBOXYLASE

<130> 07148-094001

<150> US 60/198,794

<151> 2000-04-20

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 1

caucauac auatcgatag gtaccaaaaa aaacaaccat ggcttcctca gttctt 56

<210> 2

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> primer for PCR

<400> 2

cuacuacuac uagctagcca tggacttctt gttaattggg ggcca 45

<210> 3

<211> 204

<212> DNA

<213> Nicotiana tabacum

<220>

<221> CDS

<222> (1)...(204)

<400> 3

atg gct tcc tca gtt ctt tcc tct gca gca gtt gcc acc cgc agc aat 48
Met Ala Ser Ser Val Leu Ser Ser Ala Ala Val Ala Thr Arg Ser Asn
1 5 10 15

ggt gct caa gct aac atg gtt gca cct ttc act ggc ctt aag tca gct 96
Val Ala Gln Ala Asn Met Val Ala Pro Phe Thr Gly Leu Lys Ser Ala
20 25 30

0003947 "042001

```
<210> 7
<211> 7151
```

<212> DNA
<213> Medicago sativa

<220>
<221> CDS
<222> (1)...(6771)

<400> 7

atg gct agc gtg ggc cgt gga aat gga tat tta aac agt gtg cta ccg	48
Met Ala Ser Val Gly Arg Gly Asn Gly Tyr Leu Asn Ser Val Leu Pro	
1 5 10 15	
agt agg cac cct gct act aca acc gaa gta gat gaa tac tgc aat gcc	96
Ser Arg His Pro Ala Thr Thr Thr Glu Val Asp Glu Tyr Cys Asn Ala	
20 25 30	
ctt gga gga aac aag ccg att cat agc ata ttg att gca aac aat gga	144
Leu Gly Gly Asn Lys Pro Ile His Ser Ile Leu Ile Ala Asn Asn Gly	
35 40 45	
atg gca gca gtc aag ttt ata cgt agt gtt agg agt tgg gct tac gag	192
Met Ala Ala Val Lys Phe Ile Arg Ser Val Arg Ser Trp Ala Tyr Glu	
50 55 60	
aca ttt ggc acg gaa aaa gct atc ttg ttg gtt gcc atg gca act cca	240
Thr Phe Gly Thr Glu Lys Ala Ile Leu Leu Val Ala Met Ala Thr Pro	
65 70 75 80	
gag gat atg aga atc aat gca gaa cat atc aga ata gcc gat caa ttt	288
Glu Asp Met Arg Ile Asn Ala Glu His Ile Arg Ile Ala Asp Gln Phe	
85 90 95	
gtg gaa gta cct ggt ggg acc aat aac aat aac tac gcc aat gtg cag	336
Val Glu Val Pro Gly Gly Thr Asn Asn Asn Asn Tyr Ala Asn Val Gln	
100 105 110	
ctt att cta gag att gct gag ata act cac gtt gat gcg gtg tgg cct	384
Leu Ile Leu Glu Ile Ala Glu Ile Thr His Val Asp Ala Val Trp Pro	
115 120 125	
ggt tgg ggt cat gca tca gaa aat cct gag ctt cca gat gca tta aaa	432
Gly Trp Gly His Ala Ser Glu Asn Pro Glu Leu Pro Asp Ala Leu Lys	
130 135 140	
gca aag gga att gta ttc ctt gga cct cct gct ata tct atg gca gca	480
Ala Lys Gly Ile Val Phe Leu Gly Pro Pro Ala Ile Ser Met Ala Ala	
145 150 155 160	
ttg gga gac aaa att ggt tcc tcg ttg att gct cag gca gca gaa gtt	528
Leu Gly Asp Lys Ile Gly Ser Ser Leu Ile Ala Gln Ala Ala Glu Val	
165 170 175	
cca acc ctt cca tgg agt ggt tct cat gtg aaa att cct cca gaa agt	576
Pro Thr Leu Pro Trp Ser Gly Ser His Val Lys Ile Pro Pro Glu Ser	
180 185 190	
gac ttg att act att cct gat gaa att tac cgt gca gca tgt gtt tat	624

09839477-042004

Asp	Leu	Ile	Thr	Ile	Pro	Asp	Glu	Ile	Tyr	Arg	Ala	Ala	Cys	Val	Tyr		
	195						200					205					
aca	aca	gaa	gaa	gca	att	gca	agt	tgt	caa	gta	gta	ggt	tac	cct	gca	672	
Thr	Thr	Glu	Glu	Ala	Ile	Ala	Ser	Cys	Gln	Val	Val	Gly	Tyr	Pro	Ala		
	210					215				220							
atg	att	aag	gca	tct	tgg	ggt	ggt	ggc	ggc	aaa	ggc	ata	aga	aag	gtt	720	
Met	Ile	Lys	Ala	Ser	Trp	Gly	Gly	Gly	Gly	Lys	Gly	Ile	Arg	Lys	Val		
	225				230					235					240		
cat	aat	gat	gat	gag	gtt	agg	gca	ttg	ttc	aag	caa	gtt	caa	ggt	gaa	768	
His	Asn	Asp	Asp	Glu	Val	Arg	Ala	Leu	Phe	Lys	Gln	Val	Gln	Gly	Glu		
				245					250					255			
gta	cca	ggc	tca	cct	ata	ttt	ata	atg	aaa	gtt	gct	tcc	cag	agc	cga	816	
Val	Pro	Gly	Ser	Pro	Ile	Phe	Ile	Met	Lys	Val	Ala	Ser	Gln	Ser	Arg		
			260					265					270				
cat	ctt	gaa	gtc	caa	ttg	att	tgc	gat	cag	cac	gga	aat	ttt	gca	gca	864	
His	Leu	Glu	Val	Gln	Leu	Ile	Cys	Asp	Gln	His	Gly	Asn	Phe	Ala	Ala		
		275					280					285					
ttg	cac	agc	cgt	gat	tgt	agt	gtt	caa	aga	agg	cat	caa	aag	att	att	912	
Leu	His	Ser	Arg	Asp	Cys	Ser	Val	Gln	Arg	Arg	His	Gln	Lys	Ile	Ile		
		290				295					300						
gaa	gag	ggt	ccc	att	act	gta	gca	cct	cca	gaa	acg	gtg	aaa	gaa	ctt	960	
Glu	Glu	Gly	Pro	Ile	Thr	Val	Ala	Pro	Pro	Glu	Thr	Val	Lys	Glu	Leu		
	305				310				315					320			
gaa	cag	gcg	gct	aga	aga	tta	gct	aaa	tct	gta	aat	tat	gtg	ggg	gca	1008	
Glu	Gln	Ala	Ala	Arg	Arg	Leu	Ala	Lys	Ser	Val	Asn	Tyr	Val	Gly	Ala		
				325				330						335			
gct	acc	gtt	gag	tat	ctt	tat	agc	atg	gaa	act	ggc	gag	tac	tac	ttt	1056	
Ala	Thr	Val	Glu	Tyr	Leu	Tyr	Ser	Met	Glu	Thr	Gly	Glu	Tyr	Tyr	Phe		
			340					345					350				
tta	gag	ttg	aac	ccc	cga	cta	cag	gtt	gag	cat	cct	gtt	act	gaa	tgg	1104	
Leu	Glu	Leu	Asn	Pro	Arg	Leu	Gln	Val	Glu	His	Pro	Val	Thr	Glu	Trp		
		355					360					365					
ata	gct	gag	ata	aat	ctg	cca	gca	gca	caa	gtt	gca	gtt	ggg	atg	ggc	1152	
Ile	Ala	Glu	Ile	Asn	Leu	Pro	Ala	Ala	Gln	Val	Ala	Val	Gly	Met	Gly		
	370					375					380						
atc	cca	ctc	tgg	caa	att	cct	gag	att	agg	cgt	ttc	tat	ggg	atg	gaa	1200	
Ile	Pro	Leu	Trp	Gln	Ile	Pro	Glu	Ile	Arg	Arg	Phe	Tyr	Gly	Met	Glu		
	385				390				395					400			
cat	ggt	ggg	gga	aat	gat	ggt	tgg	aag	aaa	aca	tca	gtg	tta	gct	acc	1248	
His	Gly	Gly	Gly	Asn	Asp	Gly	Trp	Lys	Lys	Thr	Ser	Val	Leu	Ala	Thr		
				405				410					415				
cct	ttt	gat	ttt	gac	gaa	gca	caa	tct	aca	aag	ccg	aaa	ggt	cat	tgt	1296	
Pro	Phe	Asp	Phe	Asp	Glu	Ala	Gln	Ser	Thr	Lys	Pro	Lys	Gly	His	Cys		

090347-0400
 100240-2450

420	425	430	
gtg gct gta cga gtc acc agt gag gac ccc gat gat ggt ttt acg cct Val Ala Val Arg Val Thr Ser Glu Asp Pro Asp Asp Gly Phe Thr Pro 435 440 445			1344
aca gga gga aaa gtg cag gag ctc agc ttt aaa agc aag cca aat gtg Thr Gly Gly Lys Val Gln Glu Leu Ser Phe Lys Ser Lys Pro Asn Val 450 455 460			1392
tgg gct tat ttc tct gtt aag tcc gga gga gga att cat gaa ttc tca Trp Ala Tyr Phe Ser Val Lys Ser Gly Gly Gly Ile His Glu Phe Ser 465 470 475 480			1440
gat tct caa ttt gga cat gtt ttt gcg ttt gga gaa tct aga gct tta Asp Ser Gln Phe Gly His Val Phe Ala Phe Gly Glu Ser Arg Ala Leu 485 490 495			1488
gca att gca aat atg gta ctg ggg ttg aag gaa att caa att cga gga Ala Ile Ala Asn Met Val Leu Gly Leu Lys Glu Ile Gln Ile Arg Gly 500 505 510			1536
gaa att cgt acc aac gtt gat tac aca att gat ctt ctg aat gct tca Glu Ile Arg Thr Asn Val Asp Tyr Thr Ile Asp Leu Leu Asn Ala Ser 515 520 525			1584
gac tac aga gac aac aaa att cac aca gga tgg cta gac agt aga att Asp Tyr Arg Asp Asn Lys Ile His Thr Gly Trp Leu Asp Ser Arg Ile 530 535 540			1632
gca atg cgg gtt aga gca gag agg cct ccc tgg tat ctg tct gtt gtt Ala Met Arg Val Arg Ala Glu Arg Pro Pro Trp Tyr Leu Ser Val Val 545 550 555 560			1680
ggt ggg gca ctc tat aaa gct tct gcc agc agt gca gct tta gtt tcg Gly Gly Ala Leu Tyr Lys Ala Ser Ala Ser Ser Ala Ala Leu Val Ser 565 570 575			1728
gac tat gtt ggc tat ctt gaa aag ggg caa atc cct ccc aag cac att Asp Tyr Val Gly Tyr Leu Glu Lys Gly Gln Ile Pro Pro Lys His Ile 580 585 590			1776
tct ctt gtc cat tct caa gtt tct ttg agc att gaa gga agc aaa tac Ser Leu Val His Ser Gln Val Ser Leu Ser Ile Glu Gly Ser Lys Tyr 595 600 605			1824
acg att gac atg gta cga gga gga cct gga agt tac aaa ttg aaa ttg Thr Ile Asp Met Val Arg Gly Gly Pro Gly Ser Tyr Lys Leu Lys Leu 610 615 620			1872
aat caa tcg gag ata gaa gcg gag ata cac act tta cgt gat gga ggt Asn Gln Ser Glu Ile Glu Ala Glu Ile His Thr Leu Arg Asp Gly Gly 625 630 635 640			1920
ttg cta atg cag ttg gat gga aac agt cat gta ata tat gca gag gaa Leu Leu Met Gln Leu Asp Gly Asn Ser His Val Ile Tyr Ala Glu Glu 645 650 655			1968

T002270" 2446860

gaa gca gct gga act cgg ctt tta ata gat gga agg act tgc ttg ctt	2016
Glu Ala Ala Gly Thr Arg Leu Leu Ile Asp Gly Arg Thr Cys Leu Leu	
660 665 670	
cag aat gat gac gat cca tca aag tta att gga gag aca ccg tgc aag	2064
Gln Asn Asp Asp Asp Pro Ser Lys Leu Ile Gly Glu Thr Pro Cys Lys	
675 680 685	
ctt ctg aga tat ttg gtt gcg gat gat agt cag att gat gca gac aca	2112
Leu Leu Arg Tyr Leu Val Ala Asp Asp Ser Gln Ile Asp Ala Asp Thr	
690 695 700	
cca tat gct gaa gtt gag gtc atg aag atg tgc atg cct ctt ctt tcc	2160
Pro Tyr Ala Glu Val Glu Val Met Lys Met Cys Met Pro Leu Leu Ser	
705 710 715 720	
cct gct tct gga att att cat ttc aga atg gct gaa ggt caa gcc atg	2208
Pro Ala Ser Gly Ile Ile His Phe Arg Met Ala Glu Gly Gln Ala Met	
725 730 735	
cag gct ggt gaa ctt ata gca aag ctt gat cta gat gat ggt tct gca	2256
Gln Ala Gly Glu Leu Ile Ala Lys Leu Asp Leu Asp Asp Gly Ser Ala	
740 745 750	
gta agg aag gca gaa ccc ttc act ggg agc ttc cct atc ctg ggc cct	2304
Val Arg Lys Ala Glu Pro Phe Thr Gly Ser Phe Pro Ile Leu Gly Pro	
755 760 765	
cct act gca att tca ggt aaa gtt cat cag aaa tgt gca gca agc tta	2352
Pro Thr Ala Ile Ser Gly Lys Val His Gln Lys Cys Ala Ala Ser Leu	
770 775 780	
aac gct gca cgg atg att ctt gct ggc tat gag cac aac att gat gaa	2400
Asn Ala Ala Arg Met Ile Leu Ala Gly Tyr Glu His Asn Ile Asp Glu	
785 790 795 800	
gtt gtg gtc aaa agt ttg ctc aat tgc ctt gac agc cct gaa ctg cct	2448
Val Val Val Lys Ser Leu Leu Asn Cys Leu Asp Ser Pro Glu Leu Pro	
805 810 815	
ttc ctt caa tgg caa gag tgc ttt gca gtt ttg gca acc cgt ctt ccc	2496
Phe Leu Gln Trp Gln Glu Cys Phe Ala Val Leu Ala Thr Arg Leu Pro	
820 825 830	
aaa gat ctt aga aac gag ttg gaa gct aaa tat aag gag ttc gaa att	2544
Lys Asp Leu Arg Asn Glu Leu Glu Ala Lys Tyr Lys Glu Phe Glu Ile	
835 840 845	
att tca agc tcc caa act att gat ttc cct gcc aaa tta ttg aag gca	2592
Ile Ser Ser Ser Gln Thr Ile Asp Phe Pro Ala Lys Leu Leu Lys Ala	
850 855 860	
atc ctt gaa gct cat ctt tcc tcc tgt cct gaa aac gaa aaa gga gcc	2640
Ile Leu Glu Ala His Leu Ser Ser Cys Pro Glu Asn Glu Lys Gly Ala	
865 870 875 880	

T00240" 245866

tta gaa aga cta gtt gaa ccg ctg aca agt ctt gta aag tct tat gag Leu Glu Arg Leu Val Glu Pro Leu Thr Ser Leu Val Lys Ser Tyr Glu 885 890 895	2688
ggt gga aga gag agc cat gct cat aaa att gtt caa tct cta ttt gaa Gly Gly Arg Glu Ser His Ala His Lys Ile Val Gln Ser Leu Phe Glu 900 905 910	2736
gag tat ctt tca gtt gaa gaa cta ttc agt gat aat ata cag gct gat Glu Tyr Leu Ser Val Glu Glu Leu Phe Ser Asp Asn Ile Gln Ala Asp 915 920 925	2784
gta att gaa cga ctc cgt ctt caa tac aag aaa gat ttg ttg aag att Val Ile Glu Arg Leu Arg Leu Gln Tyr Lys Lys Asp Leu Leu Lys Ile 930 935 940	2832
gta gat att gtg ctc tct cat cag ggt gtc aag agc aaa aac aag ctg Val Asp Ile Val Leu Ser His Gln Gly Val Lys Ser Lys Asn Lys Leu 945 950 955 960	2880
ata ctg cga cta atg gat aaa ctg gtt tac cct aat cct gct gcc tat Ile Leu Arg Leu Met Asp Lys Leu Val Tyr Pro Asn Pro Ala Ala Tyr 965 970 975	2928
agg gat caa tta atc cga ttc tcc caa ctc aac cat ata gtt tat tct Arg Asp Gln Leu Ile Arg Phe Ser Gln Leu Asn His Ile Val Tyr Ser 980 985 990	2976
gag ttg gct ctt aag gca agt caa ctg ttg gag caa act aaa ctc agt Glu Leu Ala Leu Lys Ala Ser Gln Leu Leu Glu Gln Thr Lys Leu Ser 995 1000 1005	3024
gaa ctt cga tcc agc att gct aga agt ctt tct gaa cta gaa atg ttt Glu Leu Arg Ser Ser Ile Ala Arg Ser Leu Ser Glu Leu Glu Met Phe 1010 1015 1020	3072
acc gag gat ggt gaa aat att gat act ccg aag agg aag agt gcc att Thr Glu Asp Gly Glu Asn Ile Asp Thr Pro Lys Arg Lys Ser Ala Ile 1025 1030 1035 1040	3120
aat gac aga atg gag gac ctt gtg agc gct cct ttg gct gtt gaa gat Asn Asp Arg Met Glu Asp Leu Val Ser Ala Pro Leu Ala Val Glu Asp 1045 1050 1055	3168
gcc ctt gtt ggt tta ttt gat cac agc gat cac acc ctt caa agg aga Ala Leu Val Gly Leu Phe Asp His Ser Asp His Thr Leu Gln Arg Arg 1060 1065 1070	3216
gtt gtt gaa act tat atc cgt agg ctc tat cag cca tat ctt gtc aaa Val Val Glu Thr Tyr Ile Arg Arg Leu Tyr Gln Pro Tyr Leu Val Lys 1075 1080 1085	3264
gat agc atc agg atg cag tgg cac aga tct ggc ctt att gct aca tgg Asp Ser Ile Arg Met Gln Trp His Arg Ser Gly Leu Ile Ala Thr Trp 1090 1095 1100	3312
gaa ttc tta gaa gaa tac gtt gaa cgg aag aat ggg gtt gaa gac aaa	3360

FOO247-04200

Glu Phe Leu Glu Glu Tyr Val Glu Arg Lys Asn Gly Val Glu Asp Lys	
1105	1110 1115 1120
aca ctg gtg gag aaa cat agt gag aag aaa tgg gga gtg atg gtt gta	3408
Thr Leu Val Glu Lys His Ser Glu Lys Lys Trp Gly Val Met Val Val	
	1125 1130 1135
att aaa tct ctt cag ttt ttg cca gca att atc agt gct gca tta aga	3456
Ile Lys Ser Leu Gln Phe Leu Pro Ala Ile Ile Ser Ala Ala Leu Arg	
	1140 1145 1150
gaa gca acc aat aac ttt cac gat cct ctt aaa agt ggt tct ggt gac	3504
Glu Ala Thr Asn Asn Phe His Asp Pro Leu Lys Ser Gly Ser Gly Asp	
	1155 1160 1165
tca agt aac cat ggt aat atg atg cat att gga tta gtg ggg atc aac	3552
Ser Ser Asn His Gly Asn Met Met His Ile Gly Leu Val Gly Ile Asn	
	1170 1175 1180
aac caa atg agt tta ctt caa gac agt ggt gat gag gat cag gct caa	3600
Asn Gln Met Ser Leu Leu Gln Asp Ser Gly Asp Glu Asp Gln Ala Gln	
	1185 1190 1195 1200
gaa aga att gat aag ttg gcc aaa ata ctc aga gag cag gaa ata ggg	3648
Glu Arg Ile Asp Lys Leu Ala Lys Ile Leu Arg Glu Gln Glu Ile Gly	
	1205 1210 1215
tcc ata ata cat gct gca ggt gtt gga gat att agc tgt atc ata cag	3696
Ser Ile Ile His Ala Ala Gly Val Gly Asp Ile Ser Cys Ile Ile Gln	
	1220 1225 1230
agg gat gaa ggg cgt gct cca atg agg cat tcc ttt cac tgg tca tct	3744
Arg Asp Glu Gly Arg Ala Pro Met Arg His Ser Phe His Trp Ser Ser	
	1235 1240 1245
gaa aag cta tat tat gta gag gaa cca ttg ttg ctc cat ctt gaa cct	3792
Glu Lys Leu Tyr Tyr Val Glu Glu Pro Leu Leu Leu His Leu Glu Pro	
	1250 1255 1260
ccc cta tcc att tat ctt gaa ctg gac aag ctt aag tgc tat gaa aat	3840
Pro Leu Ser Ile Tyr Leu Glu Leu Asp Lys Leu Lys Cys Tyr Glu Asn	
	1265 1270 1275 1280
att cgc tat aca cca tcc cga gat cgt caa tgg cac ctc tac aca gtt	3888
Ile Arg Tyr Thr Pro Ser Arg Asp Arg Gln Trp His Leu Tyr Thr Val	
	1285 1290 1295
gtg gat acc aag cca caa cca att caa aga atg ttt ctt cga aca ctt	3936
Val Asp Thr Lys Pro Gln Pro Ile Gln Arg Met Phe Leu Arg Thr Leu	
	1300 1305 1310
atc aga cag cca acc aca aat gaa gga tac tct tct tat caa aga ctg	3984
Ile Arg Gln Pro Thr Thr Asn Glu Gly Tyr Ser Ser Tyr Gln Arg Leu	
	1315 1320 1325
gat gca gaa acg tcc cgt acc caa ttg gct atg tct tat act tca agg	4032
Asp Ala Glu Thr Ser Arg Thr Gln Leu Ala Met Ser Tyr Thr Ser Arg	

T00240" 245550

1330	1335	1340	
agc att ttt agg tcc cta atg ggc gca atg gag gag ttg gaa ctt aac			4080
Ser Ile Phe Arg Ser Leu Met Gly Ala Met Glu Glu Leu Glu Leu Asn			
1345	1350	1355	1360
tca cac aat acc acc atc aaa tct gaa cat gct cat atg tac ctc tat			4128
Ser His Asn Thr Thr Ile Lys Ser Glu His Ala His Met Tyr Leu Tyr			
1365	1370		1375
atc ata cgc gag cag caa ata gat gat ctt gtg cct tat tcc aag aaa			4176
Ile Ile Arg Glu Gln Gln Ile Asp Asp Leu Val Pro Tyr Ser Lys Lys			
1380	1385		1390
att aac ata gaa gct ggc caa gaa gaa aca aca gtt gag gca atc ttg			4224
Ile Asn Ile Glu Ala Gly Gln Glu Glu Thr Thr Val Glu Ala Ile Leu			
1395	1400		1405
gaa gaa ctg gca cag gaa atc cat tcc tct gtt ggt gta aga atg cac			4272
Glu Glu Leu Ala Gln Glu Ile His Ser Ser Val Gly Val Arg Met His			
1410	1415		1420
aga tta ggc gtt ttc gtg tgg gaa atc aag ctc tgg att aca gca tgt			4320
Arg Leu Gly Val Phe Val Trp Glu Ile Lys Leu Trp Ile Thr Ala Cys			
1425	1430	1435	1440
gga cag gca aat ggt gct tgg agg gtc att gta aac aat gtg act ggt			4368
Gly Gln Ala Asn Gly Ala Trp Arg Val Ile Val Asn Asn Val Thr Gly			
1445	1450		1455
cat aca tgc act gta cat ata tat cga gag atg gag gat gcc acc act			4416
His Thr Cys Thr Val His Ile Tyr Arg Glu Met Glu Asp Ala Thr Thr			
1460	1465		1470
cat aaa gtg gtc tac agt tca gtc act gta aag ggt ccg ttg cat ggt			4464
His Lys Val Val Tyr Ser Ser Val Thr Val Lys Gly Pro Leu His Gly			
1475	1480		1485
gta ccg gtg aat gaa aac tat caa cct ttg gga ggt att gac cga aaa			4512
Val Pro Val Asn Glu Asn Tyr Gln Pro Leu Gly Gly Ile Asp Arg Lys			
1490	1495		1500
cgt ctt gca gcg aga aag aac agc acc aca tac tgc tat gat ttc ccc			4560
Arg Leu Ala Ala Arg Lys Asn Ser Thr Thr Tyr Cys Tyr Asp Phe Pro			
1505	1510	1515	1520
ctt gca ttt caa aca tcc ttg gaa cag tcc tgg tca ata cag cag aca			4608
Leu Ala Phe Gln Thr Ser Leu Glu Gln Ser Trp Ser Ile Gln Gln Thr			
1525	1530		1535
gga att caa aga gct aat gat aag gat ctc cta aaa gta aca gag ctt			4656
Gly Ile Gln Arg Ala Asn Asp Lys Asp Leu Leu Lys Val Thr Glu Leu			
1540	1545		1550
aaa ttt tcc gaa aaa gct ggt agt tgg ggt act tct ctt gtt cct gca			4704
Lys Phe Ser Glu Lys Ala Gly Ser Trp Gly Thr Ser Leu Val Pro Ala			
1555	1560		1565

FO00240" 245850

gag cgt ctt cct gga ctc aat gat gtt ggc atg gta gcc tgg ttg atg Glu Arg Leu Pro Gly Leu Asn Asp Val Gly Met Val Ala Trp Leu Met 1570 1575 1580	4752
gaa atg tgt acg cct aaa ttc cca tct gga agg aca ata ttg gtt gtt Glu Met Cys Thr Pro Lys Phe Pro Ser Gly Arg Thr Ile Leu Val Val 1585 1590 1595 1600	4800
tca aac gat gtg acc ttc aag gcc ggg tct ttt ggc cca aga gag gat Ser Asn Asp Val Thr Phe Lys Ala Gly Ser Phe Gly Pro Arg Glu Asp 1605 1610 1615	4848
gca ttc ttt aga gca gta act gat ctt gcc tgt gca aag aaa ata cct Ala Phe Phe Arg Ala Val Thr Asp Leu Ala Cys Ala Lys Lys Ile Pro 1620 1625 1630	4896
tta att tac ttg gca gca aat tct ggt gcc cgt tta ggt gtt gcc gag Leu Ile Tyr Leu Ala Ala Asn Ser Gly Ala Arg Leu Gly Val Ala Glu 1635 1640 1645	4944
gaa gtc aaa gct tgt ttc aaa gtt ggt tgg tct gag gaa tct aaa cct Glu Val Lys Ala Cys Phe Lys Val Gly Trp Ser Glu Glu Ser Lys Pro 1650 1655 1660	4992
gaa cat ggt ttt cag tat gta tat tta aca cct gag gat tat gct cga Glu His Gly Phe Gln Tyr Val Tyr Leu Thr Pro Glu Asp Tyr Ala Arg 1665 1670 1675 1680	5040
atc gga tca tca gtg atg gca cat gaa tta aag ctt gaa agt gga gaa Ile Gly Ser Ser Val Met Ala His Glu Leu Lys Leu Glu Ser Gly Glu 1685 1690 1695	5088
acc aga tgg gtt ata gat acc att gtt ggc aaa gaa gat gga ctg gga Thr Arg Trp Val Ile Asp Thr Ile Val Gly Lys Glu Asp Gly Leu Gly 1700 1705 1710	5136
gtt gaa aac ttg agt ggt agt ggg gcc att gcc ggt gcc tat tca agg Val Glu Asn Leu Ser Gly Ser Gly Ala Ile Ala Gly Ala Tyr Ser Arg 1715 1720 1725	5184
gca tac aag gaa acc ttt aca ttg aca tat gtt acc ggt agg act gtt Ala Tyr Lys Glu Thr Phe Thr Leu Thr Tyr Val Thr Gly Arg Thr Val 1730 1735 1740	5232
gga att ggt gct tat ctt gct agg ctt ggg atg agg tgc ata cag agg Gly Ile Gly Ala Tyr Leu Ala Arg Leu Gly Met Arg Cys Ile Gln Arg 1745 1750 1755 1760	5280
ctt gat caa cct ata att ctt acc ggg ttt tca gca tta aac aaa ctt Leu Asp Gln Pro Ile Ile Leu Thr Gly Phe Ser Ala Leu Asn Lys Leu 1765 1770 1775	5328
ctt ggt agg gag gtg tac agc tct cac atg caa ctt ggt gga ccg aaa Leu Gly Arg Glu Val Tyr Ser Ser His Met Gln Leu Gly Gly Pro Lys 1780 1785 1790	5376

atc atg gca aca aat gga gtc gtt cat ctc aca gtt tcg gac gac ctt Ile Met Ala Thr Asn Gly Val Val His Leu Thr Val Ser Asp Asp Leu 1795 1800 1805	5424
gaa ggc gtt tct tct att ttg aag tgg ctt agc tac gtt cct tct cat Glu Gly Val Ser Ser Ile Leu Lys Trp Leu Ser Tyr Val Pro Ser His 1810 1815 1820	5472
gta ggt ggt gca ctt ccc att gta aag ccc ctt gat ccc cca gag agg Val Gly Gly Ala Leu Pro Ile Val Lys Pro Leu Asp Pro Pro Glu Arg 1825 1830 1835 1840	5520
gaa gtg gag tat tta ccg gaa aat tca tgc gat cct cgt gct gcc att Glu Val Glu Tyr Leu Pro Glu Asn Ser Cys Asp Pro Arg Ala Ala Ile 1845 1850 1855	5568
tcc gga act ctg gat gtt aat gga aag tgg ctg gga ggc att ttt gac Ser Gly Thr Leu Asp Val Asn Gly Lys Trp Leu Gly Gly Ile Phe Asp 1860 1865 1870	5616
aag gac agc ttt gtg gag aca cta gaa gga tgg gct aga aca gtt gtt Lys Asp Ser Phe Val Glu Thr Leu Glu Gly Trp Ala Arg Thr Val Val 1875 1880 1885	5664
aca gga agg gca aag ctt gga gga atc cct gtg gga att gtt gcg gtg Thr Gly Arg Ala Lys Leu Gly Gly Ile Pro Val Gly Ile Val Ala Val 1890 1895 1900	5712
gaa aca caa aca gtt atg caa ata ata cct gct gat cca ggt caa ctt Glu Thr Gln Thr Val Met Gln Ile Ile Pro Ala Asp Pro Gly Gln Leu 1905 1910 1915 1920	5760
gat tct cac gag agg gtt gtt cct caa gcc ggg cag gtg tgg ttt cct Asp Ser His Glu Arg Val Val Pro Gln Ala Gly Gln Val Trp Phe Pro 1925 1930 1935	5808
gat tct gcg acc aag acg gcc caa gcg ata ttg gat ttc aac aga gaa Asp Ser Ala Thr Lys Thr Ala Gln Ala Ile Leu Asp Phe Asn Arg Glu 1940 1945 1950	5856
gaa ctc cca ctt ttc att atc gca aac tgg aga ggc ttt tca ggt gga Glu Leu Pro Leu Phe Ile Ile Ala Asn Trp Arg Gly Phe Ser Gly Gly 1955 1960 1965	5904
caa agg gac ctt ttt gaa gga att ctt cag gct ggt tcg act att gtg Gln Arg Asp Leu Phe Glu Gly Ile Leu Gln Ala Gly Ser Thr Ile Val 1970 1975 1980	5952
gag aac ctt agg aca tac aaa cag ccc ata ttt gta tac att cca atg Glu Asn Leu Arg Thr Tyr Lys Gln Pro Ile Phe Val Tyr Ile Pro Met 1985 1990 1995 2000	6000
atg ggt gaa ctc cga ggc ggg gct tgg gtt gtt gtc gac agc cga atc Met Gly Glu Leu Arg Gly Gly Ala Trp Val Val Val Asp Ser Arg Ile 2005 2010 2015	6048
aac tca gac cac att gaa atg tat gct gag cga acg gcc aaa ggt aac	6096

0933947" 042001

Asn Ser Asp His Ile Glu Met Tyr Ala Glu Arg Thr Ala Lys Gly Asn	
2020	2025 2030
gtc ctt gag ccg gaa gga atg att gaa atc aaa ttt aga aca aga gaa	6144
Val Leu Glu Pro Glu Gly Met Ile Glu Ile Lys Phe Arg Thr Arg Glu	
2035	2040 2045
ttg ttg gag tgt atg aga aga ctt gat caa caa ttg att aat ttg aag	6192
Leu Leu Glu Cys Met Arg Arg Leu Asp Gln Gln Leu Ile Asn Leu Lys	
2050	2055 2060
gaa aaa ctt tct gaa gcc aag agt aac aag gac tat ggt gca tat gat	6240
Glu Lys Leu Ser Glu Ala Lys Ser Asn Lys Asp Tyr Gly Ala Tyr Asp	
2065	2070 2075 2080
tct ctg cag cag cag att aga ttc cgt gag aaa cag ctt ttg cct ttg	6288
Ser Leu Gln Gln Gln Ile Arg Phe Arg Glu Lys Gln Leu Leu Pro Leu	
2085	2090 2095
tat act cag ata gct aca aaa ttt gct gaa ctc cat gat act tca tta	6336
Tyr Thr Gln Ile Ala Thr Lys Phe Ala Glu Leu His Asp Thr Ser Leu	
2100	2105 2110
aga atg aaa gca aag ggt gta atc aga gaa gtt ctt gat tgg cgt aag	6384
Arg Met Lys Ala Lys Gly Val Ile Arg Glu Val Leu Asp Trp Arg Lys	
2115	2120 2125
tcg cgt tct gtc ttc tat cag aga ctg cac agg aga atc ggt gag cac	6432
Ser Arg Ser Val Phe Tyr Gln Arg Leu His Arg Arg Ile Gly Glu His	
2130	2135 2140
tca ctg atc aac atc gtg aga gat gct gct ggt gac caa ttg tca tat	6480
Ser Leu Ile Asn Ile Val Arg Asp Ala Ala Gly Asp Gln Leu Ser Tyr	
2145	2150 2155 2160
gtt tct gcc atg aac ttg ctc aaa gaa tgg tat ctg aat tct gat atc	6528
Val Ser Ala Met Asn Leu Leu Lys Glu Trp Tyr Leu Asn Ser Asp Ile	
2165	2170 2175
gcc aaa ggt aga gaa gat gct tgg ttg gac gat gaa gcc ttc ttc aga	6576
Ala Lys Gly Arg Glu Asp Ala Trp Leu Asp Asp Glu Ala Phe Phe Arg	
2180	2185 2190
tgg agg gat gat cca gca aac tac gag gat aaa cta aag gaa ttg cgc	6624
Trp Arg Asp Asp Pro Ala Asn Tyr Glu Asp Lys Leu Lys Glu Leu Arg	
2195	2200 2205
gtc cag aga ctg ttg ctt cag ttg aca aat att ggc gac tcg gct cta	6672
Val Gln Arg Leu Leu Leu Gln Leu Thr Asn Ile Gly Asp Ser Ala Leu	
2210	2215 2220
gat tta caa gct cta cct caa ggt ctt gcc gcc ctt tta agc aag ttg	6720
Asp Leu Gln Ala Leu Pro Gln Gly Leu Ala Ala Leu Leu Ser Lys Leu	
2225	2230 2235 2240
gaa gca tca agt cgc gat aag ttg atc agt gaa ctt cgc aaa gta ctc	6768
Glu Ala Ser Ser Arg Asp Lys Leu Ile Ser Glu Leu Arg Lys Val Leu	

F00240" 2468660

2245

2250

2255

ggt tagtagacag tgaatgctcc tgtgatctgc ccatgcactc atgtttagt 6821
Gly

gttcacgtcg ttgatacatg accatataga aatgtatcca ttttacgatg ttatcatcaa 6881
agtagcagca tccctcggaa aatggacttt cacttgaggg atcaactgta aatgacttcg 6941
gtcttgata gatatttaat ttatgcagtt agaggatcat aaccagcatc accatgtttg 7001
gtctatttat ttgctgggtg attgattcct tgcgtgtatc tgaataaaca tgtaataatt 7061
tgtaacattg attatTTTTT atgaaaaaca aagttttggg cactcctttt ataaaaaaaa 7121
aaaaaagaat tcctgcagcc cgggggatcc 7151

<210> 8

<211> 2257

<212> PRT

<213> Medicago sativa

<400> 8

Met	Ala	Ser	Val	Gly	Arg	Gly	Asn	Gly	Tyr	Leu	Asn	Ser	Val	Leu	Pro
1				5					10					15	
Ser	Arg	His	Pro	Ala	Thr	Thr	Thr	Glu	Val	Asp	Glu	Tyr	Cys	Asn	Ala
			20					25					30		
Leu	Gly	Gly	Asn	Lys	Pro	Ile	His	Ser	Ile	Leu	Ile	Ala	Asn	Asn	Gly
			35				40						45		
Met	Ala	Ala	Val	Lys	Phe	Ile	Arg	Ser	Val	Arg	Ser	Trp	Ala	Tyr	Glu
	50					55				60					
Thr	Phe	Gly	Thr	Glu	Lys	Ala	Ile	Leu	Leu	Val	Ala	Met	Ala	Thr	Pro
65					70					75					80
Glu	Asp	Met	Arg	Ile	Asn	Ala	Glu	His	Ile	Arg	Ile	Ala	Asp	Gln	Phe
				85					90					95	
Val	Glu	Val	Pro	Gly	Gly	Thr	Asn	Asn	Asn	Asn	Tyr	Ala	Asn	Val	Gln
			100					105					110		
Leu	Ile	Leu	Glu	Ile	Ala	Glu	Ile	Thr	His	Val	Asp	Ala	Val	Trp	Pro
	115						120					125			
Gly	Trp	Gly	His	Ala	Ser	Glu	Asn	Pro	Glu	Leu	Pro	Asp	Ala	Leu	Lys
	130					135					140				
Ala	Lys	Gly	Ile	Val	Phe	Leu	Gly	Pro	Pro	Ala	Ile	Ser	Met	Ala	Ala
145					150					155					160
Leu	Gly	Asp	Lys	Ile	Gly	Ser	Ser	Leu	Ile	Ala	Gln	Ala	Ala	Glu	Val
				165					170					175	
Pro	Thr	Leu	Pro	Trp	Ser	Gly	Ser	His	Val	Lys	Ile	Pro	Pro	Glu	Ser
			180					185					190		
Asp	Leu	Ile	Thr	Ile	Pro	Asp	Glu	Ile	Tyr	Arg	Ala	Ala	Cys	Val	Tyr
	195						200					205			
Thr	Thr	Glu	Glu	Ala	Ile	Ala	Ser	Cys	Gln	Val	Val	Gly	Tyr	Pro	Ala
	210					215						220			
Met	Ile	Lys	Ala	Ser	Trp	Gly	Gly	Gly	Gly	Lys	Gly	Ile	Arg	Lys	Val
225					230					235					240
His	Asn	Asp	Asp	Glu	Val	Arg	Ala	Leu	Phe	Lys	Gln	Val	Gln	Gly	Glu
				245					250					255	
Val	Pro	Gly	Ser	Pro	Ile	Phe	Ile	Met	Lys	Val	Ala	Ser	Gln	Ser	Arg
			260					265					270		
His	Leu	Glu	Val	Gln	Leu	Ile	Cys	Asp	Gln	His	Gly	Asn	Phe	Ala	Ala
	275						280					285			
Leu	His	Ser	Arg	Asp	Cys	Ser	Val	Gln	Arg	Arg	His	Gln	Lys	Ile	Ile
	290						295					300			

F00240" 4468660

Glu Glu Gly Pro Ile Thr Val Ala Pro Pro Glu Thr Val Lys Glu Leu
 305 310 315 320
 Glu Gln Ala Ala Arg Arg Leu Ala Lys Ser Val Asn Tyr Val Gly Ala
 325 330 335
 Ala Thr Val Glu Tyr Leu Tyr Ser Met Glu Thr Gly Glu Tyr Tyr Phe
 340 345 350
 Leu Glu Leu Asn Pro Arg Leu Gln Val Glu His Pro Val Thr Glu Trp
 355 360 365
 Ile Ala Glu Ile Asn Leu Pro Ala Ala Gln Val Ala Val Gly Met Gly
 370 375 380
 Ile Pro Leu Trp Gln Ile Pro Glu Ile Arg Arg Phe Tyr Gly Met Glu
 385 390 395 400
 His Gly Gly Gly Asn Asp Gly Trp Lys Lys Thr Ser Val Leu Ala Thr
 405 410 415
 Pro Phe Asp Phe Asp Glu Ala Gln Ser Thr Lys Pro Lys Gly His Cys
 420 425 430
 Val Ala Val Arg Val Thr Ser Glu Asp Pro Asp Asp Gly Phe Thr Pro
 435 440 445
 Thr Gly Gly Lys Val Gln Glu Leu Ser Phe Lys Ser Lys Pro Asn Val
 450 455 460
 Trp Ala Tyr Phe Ser Val Lys Ser Gly Gly Gly Ile His Glu Phe Ser
 465 470 475 480
 Asp Ser Gln Phe Gly His Val Phe Ala Phe Gly Glu Ser Arg Ala Leu
 485 490 495
 Ala Ile Ala Asn Met Val Leu Gly Leu Lys Glu Ile Gln Ile Arg Gly
 500 505 510
 Glu Ile Arg Thr Asn Val Asp Tyr Thr Ile Asp Leu Leu Asn Ala Ser
 515 520 525
 Asp Tyr Arg Asp Asn Lys Ile His Thr Gly Trp Leu Asp Ser Arg Ile
 530 535 540
 Ala Met Arg Val Arg Ala Glu Arg Pro Pro Trp Tyr Leu Ser Val Val
 545 550 555 560
 Gly Gly Ala Leu Tyr Lys Ala Ser Ala Ser Ser Ala Ala Leu Val Ser
 565 570 575
 Asp Tyr Val Gly Tyr Leu Glu Lys Gly Gln Ile Pro Pro Lys His Ile
 580 585 590
 Ser Leu Val His Ser Gln Val Ser Leu Ser Ile Glu Gly Ser Lys Tyr
 595 600 605
 Thr Ile Asp Met Val Arg Gly Gly Pro Gly Ser Tyr Lys Leu Lys Leu
 610 615 620
 Asn Gln Ser Glu Ile Glu Ala Glu Ile His Thr Leu Arg Asp Gly Gly
 625 630 635 640
 Leu Leu Met Gln Leu Asp Gly Asn Ser His Val Ile Tyr Ala Glu Glu
 645 650 655
 Glu Ala Ala Gly Thr Arg Leu Leu Ile Asp Gly Arg Thr Cys Leu Leu
 660 665 670
 Gln Asn Asp Asp Asp Pro Ser Lys Leu Ile Gly Glu Thr Pro Cys Lys
 675 680 685
 Leu Leu Arg Tyr Leu Val Ala Asp Asp Ser Gln Ile Asp Ala Asp Thr
 690 695 700
 Pro Tyr Ala Glu Val Glu Val Met Lys Met Cys Met Pro Leu Leu Ser
 705 710 715 720
 Pro Ala Ser Gly Ile Ile His Phe Arg Met Ala Glu Gly Gln Ala Met
 725 730 735
 Gln Ala Gly Glu Leu Ile Ala Lys Leu Asp Leu Asp Asp Gly Ser Ala
 740 745 750
 Val Arg Lys Ala Glu Pro Phe Thr Gly Ser Phe Pro Ile Leu Gly Pro

FOUO247-042001

[illegible]

Ser Ile Ile His Ala Ala Gly Val Gly Asp Ile Ser Cys Ile Ile Gln
 1220 1225 1230
 Arg Asp Glu Gly Arg Ala Pro Met Arg His Ser Phe His Trp Ser Ser
 1235 1240 1245
 Glu Lys Leu Tyr Tyr Val Glu Glu Pro Leu Leu Leu His Leu Glu Pro
 1250 1255 1260
 Pro Leu Ser Ile Tyr Leu Glu Leu Asp Lys Leu Lys Cys Tyr Glu Asn
 1265 1270 1275 1280
 Ile Arg Tyr Thr Pro Ser Arg Asp Arg Gln Trp His Leu Tyr Thr Val
 1285 1290 1295
 Val Asp Thr Lys Pro Gln Pro Ile Gln Arg Met Phe Leu Arg Thr Leu
 1300 1305 1310
 Ile Arg Gln Pro Thr Thr Asn Glu Gly Tyr Ser Ser Tyr Gln Arg Leu
 1315 1320 1325
 Asp Ala Glu Thr Ser Arg Thr Gln Leu Ala Met Ser Tyr Thr Ser Arg
 1330 1335 1340
 Ser Ile Phe Arg Ser Leu Met Gly Ala Met Glu Glu Leu Glu Leu Asn
 1345 1350 1355 1360
 Ser His Asn Thr Thr Ile Lys Ser Glu His Ala His Met Tyr Leu Tyr
 1365 1370 1375
 Ile Ile Arg Glu Gln Gln Ile Asp Asp Leu Val Pro Tyr Ser Lys Lys
 1380 1385 1390
 Ile Asn Ile Glu Ala Gly Gln Glu Glu Thr Thr Val Glu Ala Ile Leu
 1395 1400 1405
 Glu Glu Leu Ala Gln Glu Ile His Ser Ser Val Gly Val Arg Met His
 1410 1415 1420
 Arg Leu Gly Val Phe Val Trp Glu Ile Lys Leu Trp Ile Thr Ala Cys
 1425 1430 1435 1440
 Gly Gln Ala Asn Gly Ala Trp Arg Val Ile Val Asn Asn Val Thr Gly
 1445 1450 1455
 His Thr Cys Thr Val His Ile Tyr Arg Glu Met Glu Asp Ala Thr Thr
 1460 1465 1470
 His Lys Val Val Tyr Ser Ser Val Thr Val Lys Gly Pro Leu His Gly
 1475 1480 1485
 Val Pro Val Asn Glu Asn Tyr Gln Pro Leu Gly Gly Ile Asp Arg Lys
 1490 1495 1500
 Arg Leu Ala Ala Arg Lys Asn Ser Thr Thr Tyr Cys Tyr Asp Phe Pro
 1505 1510 1515 1520
 Leu Ala Phe Gln Thr Ser Leu Glu Gln Ser Trp Ser Ile Gln Gln Thr
 1525 1530 1535
 Gly Ile Gln Arg Ala Asn Asp Lys Asp Leu Leu Lys Val Thr Glu Leu
 1540 1545 1550
 Lys Phe Ser Glu Lys Ala Gly Ser Trp Gly Thr Ser Leu Val Pro Ala
 1555 1560 1565
 Glu Arg Leu Pro Gly Leu Asn Asp Val Gly Met Val Ala Trp Leu Met
 1570 1575 1580
 Glu Met Cys Thr Pro Lys Phe Pro Ser Gly Arg Thr Ile Leu Val Val
 1585 1590 1595 1600
 Ser Asn Asp Val Thr Phe Lys Ala Gly Ser Phe Gly Pro Arg Glu Asp
 1605 1610 1615
 Ala Phe Phe Arg Ala Val Thr Asp Leu Ala Cys Ala Lys Lys Ile Pro
 1620 1625 1630
 Leu Ile Tyr Leu Ala Ala Asn Ser Gly Ala Arg Leu Gly Val Ala Glu
 1635 1640 1645
 Glu Val Lys Ala Cys Phe Lys Val Gly Trp Ser Glu Glu Ser Lys Pro
 1650 1655 1660
 Glu His Gly Phe Gln Tyr Val Tyr Leu Thr Pro Glu Asp Tyr Ala Arg

T00240" 245E00

1665		1670		1675		1680
Ile Gly Ser Ser Val Met Ala His Glu Leu Lys Leu Glu Ser Gly Glu						
	1685		1690		1695	
Thr Arg Trp Val Ile Asp Thr Ile Val Gly Lys Glu Asp Gly Leu Gly						
	1700		1705		1710	
Val Glu Asn Leu Ser Gly Ser Gly Ala Ile Ala Gly Ala Tyr Ser Arg						
	1715		1720		1725	
Ala Tyr Lys Glu Thr Phe Thr Leu Thr Tyr Val Thr Gly Arg Thr Val						
	1730		1735		1740	
Gly Ile Gly Ala Tyr Leu Ala Arg Leu Gly Met Arg Cys Ile Gln Arg						
1745	1750		1755		1760	
Leu Asp Gln Pro Ile Ile Leu Thr Gly Phe Ser Ala Leu Asn Lys Leu						
	1765		1770		1775	
Leu Gly Arg Glu Val Tyr Ser Ser His Met Gln Leu Gly Gly Pro Lys						
	1780		1785		1790	
Ile Met Ala Thr Asn Gly Val Val His Leu Thr Val Ser Asp Asp Leu						
	1795		1800		1805	
Glu Gly Val Ser Ser Ile Leu Lys Trp Leu Ser Tyr Val Pro Ser His						
	1810		1815		1820	
Val Gly Gly Ala Leu Pro Ile Val Lys Pro Leu Asp Pro Pro Glu Arg						
1825	1830		1835		1840	
Glu Val Glu Tyr Leu Pro Glu Asn Ser Cys Asp Pro Arg Ala Ala Ile						
	1845		1850		1855	
Ser Gly Thr Leu Asp Val Asn Gly Lys Trp Leu Gly Gly Ile Phe Asp						
	1860		1865		1870	
Lys Asp Ser Phe Val Glu Thr Leu Glu Gly Trp Ala Arg Thr Val Val						
	1875		1880		1885	
Thr Gly Arg Ala Lys Leu Gly Gly Ile Pro Val Gly Ile Val Ala Val						
	1890		1895		1900	
Glu Thr Gln Thr Val Met Gln Ile Ile Pro Ala Asp Pro Gly Gln Leu						
1905	1910		1915		1920	
Asp Ser His Glu Arg Val Val Pro Gln Ala Gly Gln Val Trp Phe Pro						
	1925		1930		1935	
Asp Ser Ala Thr Lys Thr Ala Gln Ala Ile Leu Asp Phe Asn Arg Glu						
	1940		1945		1950	
Glu Leu Pro Leu Phe Ile Ile Ala Asn Trp Arg Gly Phe Ser Gly Gly						
	1955		1960		1965	
Gln Arg Asp Leu Phe Glu Gly Ile Leu Gln Ala Gly Ser Thr Ile Val						
	1970		1975		1980	
Glu Asn Leu Arg Thr Tyr Lys Gln Pro Ile Phe Val Tyr Ile Pro Met						
1985	1990		1995		2000	
Met Gly Glu Leu Arg Gly Gly Ala Trp Val Val Val Asp Ser Arg Ile						
	2005		2010		2015	
Asn Ser Asp His Ile Glu Met Tyr Ala Glu Arg Thr Ala Lys Gly Asn						
	2020		2025		2030	
Val Leu Glu Pro Glu Gly Met Ile Glu Ile Lys Phe Arg Thr Arg Glu						
	2035		2040		2045	
Leu Leu Glu Cys Met Arg Arg Leu Asp Gln Gln Leu Ile Asn Leu Lys						
	2050		2055		2060	
Glu Lys Leu Ser Glu Ala Lys Ser Asn Lys Asp Tyr Gly Ala Tyr Asp						
2065	2070		2075		2080	
Ser Leu Gln Gln Gln Ile Arg Phe Arg Glu Lys Gln Leu Leu Pro Leu						
	2085		2090		2095	
Tyr Thr Gln Ile Ala Thr Lys Phe Ala Glu Leu His Asp Thr Ser Leu						
	2100		2105		2110	
Arg Met Lys Ala Lys Gly Val Ile Arg Glu Val Leu Asp Trp Arg Lys						
	2115		2120		2125	

100240" 245860

Ser Arg Ser Val Phe Tyr Gln Arg Leu His Arg Arg Ile Gly Glu His
 2130 2135 2140
 Ser Leu Ile Asn Ile Val Arg Asp Ala Ala Gly Asp Gln Leu Ser Tyr
 2145 2150 2155 2160
 Val Ser Ala Met Asn Leu Leu Lys Glu Trp Tyr Leu Asn Ser Asp Ile
 2165 2170 2175
 Ala Lys Gly Arg Glu Asp Ala Trp Leu Asp Asp Glu Ala Phe Phe Arg
 2180 2185 2190
 Trp Arg Asp Asp Pro Ala Asn Tyr Glu Asp Lys Leu Lys Glu Leu Arg
 2195 2200 2205
 Val Gln Arg Leu Leu Leu Gln Leu Thr Asn Ile Gly Asp Ser Ala Leu
 2210 2215 2220
 Asp Leu Gln Ala Leu Pro Gln Gly Leu Ala Ala Leu Leu Ser Lys Leu
 2225 2230 2235 2240
 Glu Ala Ser Ser Arg Asp Lys Leu Ile Ser Glu Leu Arg Lys Val Leu
 2245 2250 2255
 Gly

<210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 9
 gtaggcaccc tgctactaca

20

<210> 10
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for PCR

<400> 10
 catcaggaat agtaatcaag tca

23

<210> 11
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> representative construct (3' end)

<400> 11
 ccttttataa aaaaaaaaaa aagaattcct gcagcccggg ggatcc

46

<210> 12
 <211> 46
 <212> DNA
 <213> Artificial Sequence

TCOCHQ " ZCHCEBEO

<220>

<223> representative construct (3' end)

<400> 12

ccttttataa aaaaaaaaaa aagaattcct gcagcccggg ggatcc

46

T00240" 246860